APPENDIX OF CLAIMS (1-11, 39-43, 45-46 AND 48)

1. A method of assaying for risk of developing hereditary lymphedema, comprising assaying nucleic acid of a human subject for a mutation that alters the encoded amino acid sequence of at least one VEGFR-3 allele of the human subject and reduces ligand-mediated signaling of the VEGFR-3 polypeptide encoded by the allele, when compared to VEGFR-3 encoded by a wild-type human VEGFR-3 allele;

wherein presence of said mutation in the nucleic acid correlates with an increased risk of developing hereditary lymphedema, and wherein absence of said mutation in the nucleic acid correlates with no increased risk of developing hereditary lymphedema.

2. A method according to claim 1 wherein the assaying step comprises assaying for a mutation altering a tyrosine kinase domain amino acid sequence of the protein encoded by the VEGFR-3 allele.

3. A method according to claim 1 wherein the assaying step comprises assaying for a missense mutation in a VEGFR-3 allele at a position corresponding to one of codons 857, 1041, 1044 and 1049 of the VEGFR-3-encoding sequence set forth in SEQ ID NO:1.

4. A method according to claim 1 wherein the assaying step comprises assaying for a missense mutation in a VEGFR-3 allele at a position corresponding to codon 1114 of the VEGFR-3-encoding sequence set forth in SEQ ID NO:1.

5. A method according to claim 1 wherein said method comprises at least one procedure selected from the group consisting of:

(a) determining a nucleotide sequence of at least one codon of at least one VEGFR-3 allele of the human subject;

(b) performing a hybridization assay to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences;

(c) performing a polynucleotide migration assay to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences; and

(d) performing a restriction endonuclease digestion to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences.

6. A method according to claim 1 wherein said method comprises: performing a polymerase chain reaction (PCR) to amplify nucleic acid comprising VEGFR-3 coding sequence, and determining nucleotide sequence of the amplified nucleic acid.

7. A method of screening for a VEGFR-3 hereditary lymphedema genotype in a human subject, comprising the steps of:

(a) providing a biological sample comprising nucleic acid from said subject, said nucleic acid including sequences corresponding to said subject's VEGFR-3 alleles;

(b) determining a VEGFR-3 genotype by analyzing said nucleic acid for the presence of a mutation altering the encoded amino acid sequence of at least one VEGFR-3 allele, wherein the presence of a mutation altering the encoded amino acid sequence of at least one VEGFR-3 allele of the human subject in a manner that reduces signaling of the VEGFR-3 polypeptide encoded by the allele, when compared to VEGFR-3 encoded by a wild-type human VEGFR-3 allele, identifies a hereditary lymphedema genotype.

8. The method according to claim 7 wherein said biological sample is a cell sample.

9. The method according to claim 7 wherein said analyzing comprises sequencing a portion of said nucleic acid, said portion comprising at least one codon of said VEGFR-3 alleles.

10. The method according to claim 7 wherein said nucleic acid is DNA.

11. The method according to claim 7 wherein said nucleic acid is RNA.

37. (Canceled)

38. (Canceled)

39. A method according to claim 1, wherein the assaying identifies the presence of the mutation, and the method identifies the increased risk of said patient developing hereditary lymphedema from the presence of the mutation.

40. A method according to claim 2 wherein the assaying identifies a mutation altering a tyrosine kinase domain amino acid sequence of the protein encoded by the VEGFR-3 allele.

41. A method according to claim 3 wherein the assaying identifies the missense mutation in a VEGFR-3 allele in the human subject.

42. A method according to claim 4 wherein the assaying identifies the missense mutation in a VEGFR-3 allele in the human subject.

43. A method according to claim 7 wherein the human subject has a hereditary lymphedema genotype identified by the method of screening.

44. (Canceled)

45. (Previously presented) A method according to claim 1, wherein the wildtype VEGFR-3 allele comprises the VEGFR-3 coding sequence set forth in SEQ ID NO: 1.

46. (Previously presented) A method according to claim 7, wherein the wildtype VEGFR-3 allele comprises the VEGFR-3 coding sequence set forth in SEQ ID NO: 1.

47. (Canceled)

48. A method of assaying for risk of developing hereditary lymphedema, comprising:

assaying nucleic acid of a human subject for a mutation that alters the encoded amino acid sequence of at least one VEGFR-3 allele of the human subject, relative to the amino acid sequence of VEGFR-3 encoded by SEQ ID NO: 1;

measuring ligand-mediated signaling of the VEGFR-3 polypeptide encoded by the allele of the human subject, relative to ligand-mediated signaling of VEGFR-3 encoded by SEQ ID NO: 1;

wherein presence of a mutation in the nucleic acid that alters the encoded amino acid sequence and reduces ligand-mediated signaling of the encoded VEGFR-3 polypeptide correlates with an increased risk of developing hereditary lymphedema, and wherein absence of said mutation correlates with no increased risk of developing hereditary lymphedema.